

RAW SEQUENCE LISTING

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Application Serial Number: 10/539,723
Source: PCT/0
Date Processed by STIC: 7/12/05

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/539,723

DATE: 07/12/2005

TIME: 10:02:55

Input Set : N:\RJAVED\10539723.txt

Output Set: N:\CRF4\07122005\J539723.raw

3 <110> APPLICANT: Bayer CropScience GmbH
 5 <120> TITLE OF INVENTION: Plant cells and plants which synthesize a starch with an increased final viscosity
 6 <130> FILE REFERENCE: BCS 02 5002 - PCT
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/539,723
 C--> 10 <141> CURRENT FILING DATE: 2005-06-20
 10 <150> PRIOR APPLICATION NUMBER: EP 02028530.0
 11 <151> PRIOR FILING DATE: 2002-12-19
 13 <150> PRIOR APPLICATION NUMBER: EP 03090275.3
 14 <151> PRIOR FILING DATE: 2003-08-29
 16 <160> NUMBER OF SEQ ID NOS: 8
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 4167
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Solanum tuberosum
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (207)..(3899)
 28 <223> OTHER INFORMATION:
 31 <300> PUBLICATION INFORMATION:
 32 <301> AUTHORS: Abel,G.J., Springer,F., Willmitzer,L. and Kossmann,J.
 33 <302> TITLE: Cloning and functional analysis of a cDNA encoding a novel 139 kDa
 34 <303> JOURNAL: Plant J.
 35 <304> VOLUME: 10
 36 <305> ISSUE: 6
 37 <306> PAGES: 981-991
 38 <307> DATE: 1996
 39 <308> DATABASE ACCESSION NO: X94400
 40 <309> DATABASE ENTRY DATE: 1995-12-22
 41 <313> RELEVANT RESIDUES: (1)..(4167)
 43 <300> PUBLICATION INFORMATION:
 44 <308> DATABASE ACCESSION NO: EMBL / X94400
 45 <309> DATABASE ENTRY DATE: 1997-04-16
 46 <313> RELEVANT RESIDUES: (1)..(4167)
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 53 gatgttctat ttgattctgt ggtgaacaag agttttacaa agaacattcc tttttctttt 180
 55 ttcttggtt cttgtgtggg tcagcc atg gat gtt cca ttt cca ctg cat aga 233
 56 Met Asp Val Pro Phe Pro Leu His Arg
 57 1 5
 59 cca ttg agt tgc aca agt gtc tcc aat gca ata acc cac ctc aag atc 281

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60 Pro Leu Ser Cys Thr Ser Val Ser Asn Ala Ile Thr His Leu Lys Ile			
61 10	15	20	25
63 aaa cct ttt ctt ggg ttt gtc tct cat gga acc aca agt cta tca gta			329
64 Lys Pro Phe Leu Gly Phe Val Ser His Gly Thr Thr Ser Leu Ser Val			
65	30	35	40
67 caa tct tct tca tgg agg aag gat gga atg gtt act ggg gtt tca ttt			377
68 Gln Ser Ser Ser Trp Arg Lys Asp Gly Met Val Thr Gly Val Ser Phe			
69	45	50	55
71 cca ttt tgt gca aat ctc tcg gga aga aga cgg aga aaa gtt tca act			425
72 Pro Phe Cys Ala Asn Leu Ser Gly Arg Arg Arg Arg Lys Val Ser Thr			
73	60	65	70
75 act agg agt caa gga tct tca cct aag ggg ttt gtg cca agg aag ccc			473
76 Thr Arg Ser Gln Gly Ser Ser Pro Lys Gly Phe Val Pro Arg Lys Pro			
77	75	80	85
79 tca ggg atg agc acg caa aga aag gtt cag aag agc aat ggt gat aaa			521
80 Ser Gly Met Ser Thr Gln Arg Lys Val Gln Lys Ser Asn Gly Asp Lys			
81 90	95	100	105
83 gaa agt caa agt act tca aca tct aaa gaa tct gaa att tcc aac cag			569
84 Glu Ser Gln Ser Thr Ser Lys Glu Ser Glu Ile Ser Asn Gln			
85	110	115	120
87 aag acg gtt gaa gca aga gtt gaa act agt gac gat gac act aaa gta			617
88 Lys Thr Val Glu Ala Arg Val Glu Thr Ser Asp Asp Asp Thr Lys Val			
89	125	130	135
91 gtg gtg agg gac cac aag ttt ctg gag gat gag gat gaa atc aat ggt			665
92 Val Val Arg Asp His Lys Phe Leu Glu Asp Glu Asp Glu Ile Asn Gly			
93	140	145	150
95 tct act aaa tca ata agt atg tca cct gtt cgt gta tca tct caa ttt			713
96 Ser Thr Lys Ser Ile Ser Met Ser Pro Val Arg Val Ser Ser Gln Phe			
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99 gtt gaa agt gaa gaa act ggt ggt gat gac aag gat gct gta aag tta			761
100 Val Glu Ser Glu Glu Thr Gly Gly Asp Asp Lys Asp Ala Val Lys Leu			
101 170	175	180	185
103 aac aaa tca aag aga tcg gaa gag agt gat ttt cta att gat tct gta			809
104 Asn Lys Ser Lys Arg Ser Glu Glu Ser Asp Phe Leu Ile Asp Ser Val			
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107 ata aga gaa caa agt gga tct cag ggg gaa act aat gcc agt agc aag			857
108 Ile Arg Glu Gln Ser Gly Ser Gln Gly Glu Thr Asn Ala Ser Ser Lys			
109	205	210	215
111 gga agc cat gct gtg ggt aca aaa ctt tat gag ata ttg cag gtg gat			905
112 Gly Ser His Ala Val Gly Thr Lys Leu Tyr Glu Ile Leu Gln Val Asp			
113	220	225	230
115 gtt gag cca caa ttg aaa gaa aat aat gct ggg aat gtt gaa tac			953
116 Val Glu Pro Gln Gln Leu Lys Glu Asn Asn Ala Gly Asn Val Glu Tyr			
117	235	240	245
119 aaa gga cct gta gca agt aag cta ttg gaa att act aag gct agt gat			1001
120 Lys Gly Pro Val Ala Ser Lys Leu Leu Glu Ile Thr Lys Ala Ser Asp			
121 250	255	260	265
123 gtg gaa cac act gaa agc aat gag att gat gac tta gac act aat agt			1049
124 Val Glu His Thr Glu Ser Asn Glu Ile Asp Asp Leu Asp Thr Asn Ser			

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128 Phe Phe Lys Ser Asp Leu Ile Glu Glu Asp Glu Pro Leu Ala Ala Gly				
129 285	290	295		
131 aca gtg gag act gga gat tct tct cta aac tta aga ttg gag atg gaa				1145
132 Thr Val Glu Thr Gly Asp Ser Ser Leu Asn Leu Arg Leu Glu Met Glu				
133 300	305	310		
135 gca aat cta cgt agg cag gct ata gaa agg ctt gcc gag gaa aat tta				1193
136 Ala Asn Leu Arg Arg Gln Ala Ile Glu Arg Leu Ala Glu Glu Asn Leu				
137 315	320	325		
139 ttg caa ggg atc aga tta ttt tgt ttt cca gag gtt gta aaa cct gat				1241
140 Leu Gln Gly Ile Arg Leu Phe Cys Phe Pro Glu Val Val Lys Pro Asp				
141 330	335	340	345	
143 gaa gat gtc gag ata ttt ctt aac aga ggt ctt tcc act ttg aag aat				1289
144 Glu Asp Val Glu Ile Phe Leu Asn Arg Gly Leu Ser Thr Leu Lys Asn				
145 350	355	360		
147 gag tct gat gtc ttg att atg gga gct ttt aat gag tgg cgc tat agg				1337
148 Glu Ser Asp Val Leu Ile Met Gly Ala Phe Asn Glu Trp Arg Tyr Arg				
149 365	370	375		
151 tct ttt act aca agg cta act gag act cat ctc aat gga gat tgg tgg				1385
152 Ser Phe Thr Thr Arg Leu Thr Glu Thr His Leu Asn Gly Asp Trp Trp				
153 380	385	390		
155 tct tgc aag atc cat gtt ccc aag gaa gca tac agg gct gat ttt gtg				1433
156 Ser Cys Lys Ile His Val Pro Lys Glu Ala Tyr Arg Ala Asp Phe Val				
157 395	400	405		
159 ttt ttt aat gga caa gat gtc tat gac aac aat gat gga aat gac ttc				1481
160 Phe Phe Asn Gly Gln Asp Val Tyr Asp Asn Asn Asp Gly Asn Asp Phe				
161 410	415	420	425	
163 agt ata act gtg aaa ggt ggt atg caa atc att gac ttt gaa aat ttc				1529
164 Ser Ile Thr Val Lys Gly Gly Met Gln Ile Ile Asp Phe Glu Asn Phe				
165 430	435	440		
167 ttg ctt gag gag aaa tgg aga gaa cag gag aaa ctt gct aaa gaa caa				1577
168 Leu Leu Glu Glu Lys Trp Arg Glu Gln Glu Lys Leu Ala Lys Glu Gln				
169 445	450	455		
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172 Ala Glu Arg Glu Arg Leu Ala Glu Glu Gln Arg Arg Ile Glu Ala Glu				
173 460	465	470		
175 aaa gct gaa att gaa gct gac aga gca caa gca aag gaa gag gac gct gca				1673
176 Lys Ala Glu Ile Glu Ala Asp Arg Ala Gln Ala Lys Glu Glu Ala Ala				
177 475	480	485		
179 aag aaa aag aaa gta ttg cga gaa ttg atg gta aaa gcc acg aag act				1721
180 Lys Lys Lys Val Leu Arg Glu Leu Met Val Lys Ala Thr Lys Thr				
181 490	495	500	505	
183 cgt gat atc acg tgg tac ata gag cca agt gaa ttt aaa tgc gag gac				1769
184 Arg Asp Ile Thr Trp Tyr Ile Glu Pro Ser Glu Phe Lys Cys Glu Asp				
185 510	515	520		
187 aag gtc agg tta tac tat aac aaa agt tca ggt cct ctc tcc cat gct				1817
188 Lys Val Arg Leu Tyr Tyr Asn Lys Ser Ser Gly Pro Leu Ser His Ala				
189 525	530	535		

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191 aag gac ttg atc cac gga gga tat aat aat tgg aag gat ggt ttg	1865
192 Lys Asp Leu Trp Ile His Gly Gly Tyr Asn Asn Trp Lys Asp Gly Leu	
193 540 545 550	
195 tct att gtc aaa aag ctt gtt aaa tct gag aga ata gat ggt gat tgg	1913
196 Ser Ile Val Lys Lys Leu Val Lys Ser Glu Arg Ile Asp Gly Asp Trp	
197 555 560 565	
199 tgg tat aca gag gtt gtt att cct gat cag gca ctt ttc ttg gat tgg	1961
200 Trp Tyr Thr Glu Val Val Ile Pro Asp Gln Ala Leu Phe Leu Asp Trp	
201 570 575 580 585	
203 gtt ttt gct gat ggt cca ccc aag cat gcc att gct tat gat aac aat	2009
204 Val Phe Ala Asp Gly Pro Pro Lys His Ala Ile Ala Tyr Asp Asn Asn	
205 590 595 600	
207 cac cgc caa gac ttc cat gcc att gtc ccc aac cac att ccg gag gaa	2057
208 His Arg Gln Asp Phe His Ala Ile Val Pro Asn His Ile Pro Glu Glu	
209 605 610 615	
211 tta tat tgg gtt gag gaa gaa cat cag atc ttt aag aca ctt cag gag	2105
212 Leu Tyr Trp Val Glu Glu His Gln Ile Phe Lys Thr Leu Gln Glu	
213 620 625 630	
215 gag aga agg ctt aga gaa gcg gct atg cgt gct aag gtt gaa aaa aca	2153
216 Glu Arg Arg Leu Arg Glu Ala Ala Met Arg Ala Lys Val Glu Lys Thr	
217 635 640 645	
219 gca ctt ctg aaa act gaa aca aag gaa aga act atg aaa tca ttt tta	2201
220 Ala Leu Leu Lys Thr Glu Thr Lys Glu Arg Thr Met Lys Ser Phe Leu	
221 650 655 660 665	
223 ctg tct cag aag cat gta gta tat act gag cct ctt gat atc caa gct	2249
224 Leu Ser Gln Lys His Val Val Tyr Thr Glu Pro Leu Asp Ile Gln Ala	
225 670 675 680	
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228 Gly Ser Ser Val Thr Val Tyr Tyr Asn Pro Ala Asn Thr Val Leu Asn	
229 685 690 695	
231 ggt aaa cct gaa att tgg ttc aga tgt tca ttt aat cgc tgg act cac	2345
232 Gly Lys Pro Glu Ile Trp Phe Arg Cys Ser Phe Asn Arg Trp Thr His	
233 700 705 710	
235 cgc ctg ggt cca ttg cca cct cag aaa atg tcg cct gct gaa aat ggc	2393
236 Arg Leu Gly Pro Leu Pro Pro Gln Lys Met Ser Pro Ala Glu Asn Gly	
237 715 720 725	
239 acc cat gtc aga gca act gtg aag gtt cca ttg gat gca tat atg atg	2441
240 Thr His Val Arg Ala Thr Val Lys Val Pro Leu Asp Ala Tyr Met Met	
241 730 735 740 745	
243 gat ttt gta ttt tcc gag aga gaa gat ggt ggg att ttt gac aat aag	2489
244 Asp Phe Val Phe Ser Glu Arg Glu Asp Gly Gly Ile Phe Asp Asn Lys	
245 750 755 760	
247 agc gga atg gac tat cac ata cct gtg ttt gga gga gtc gct aaa gaa	2537
248 Ser Gly Met Asp Tyr His Ile Pro Val Phe Gly Gly Val Ala Lys Glu	
249 765 770 775	
251 cct cca atg cat att gtc cat att gct gtc gaa atg gca cca att gca	2585
252 Pro Pro Met His Ile Val His Ile Ala Val Glu Met Ala Pro Ile Ala	
253 780 785 790	
255 aag gtg gga ggc ctt ggt gat gtt act agt ctt tcc cgt gct gtt	2633

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265						830				835				840		
267	tgg	ggg	act	gaa	ata	aaa	gta	tgg	ttt	gga	aag	gtg	gaa	ggt	ctc	
268	Trp	Gly	Gly	Thr	Glu	Ile	Lys	Val	Trp	Phe	Gly	Lys	Val	Glu	Gly	Leu
269						845			850			855				
271	tcg	gtc	tat	ttt	ttg	gag	cct	caa	aac	ggg	tta	ttt	tcg	aaa	ggg	tgc
272	Ser	Val	Tyr	Phe	Leu	Glu	Pro	Gln	Asn	Gly	Leu	Phe	Ser	Lys	Gly	Cys
273						860			865			870				
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276	Val	Tyr	Gly	Cys	Ser	Asn	Asp	Gly	Glu	Arg	Phe	Gly	Phe	Phe	Cys	His
277						875			880			885				
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280	Ala	Ala	Leu	Glu	Phe	Leu	Leu	Gln	Gly	Gly	Phe	Ser	Pro	Asp	Ile	Ile
281	890				895					900			905			
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288	Gln	Tyr	Thr	His	Tyr	Gly	Leu	Ser	Lys	Ser	Arg	Ile	Val	Phe	Thr	Ile
289						925			930			935				
291	cat	aat	ctt	gaa	ttt	ggg	gca	gat	ctc	att	ggg	aga	gca	atg	act	aac
292	His	Asn	Leu	Glu	Phe	Gly	Ala	Asp	Leu	Ile	Gly	Arg	Ala	Met	Thr	Asn
293						940			945			950				
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297						955			960			965				
299	gga	aac	cct	gta	att	gct	cct	cac	cac	aag	ttc	cat	ggt	ata	gtg	
300	Gly	Asn	Pro	Val	Ile	Ala	Pro	His	Leu	His	Lys	Phe	His	Gly	Ile	Val
301	970				975					980			985			
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304	Asn	Gly	Ile	Asp	Pro	Asp	Ile	Trp	Asp	Pro	Leu	Asn	Asp	Lys	Phe	Ile
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312	Ala	Lys	Glu	Ala	Leu	Gln	Arg	Lys	Leu	Gly	Leu	Lys	Gln	Ala	Asp	
313						1020				1025			1030			
315	ctt	cct	ttg	gta	gga	att	atc	acc	cgc	tta	act	cac	cag	aaa	gga	
316	Leu	Pro	Leu	Val	Gly	Ile	Ile	Thr	Arg	Leu	Thr	His	Gln	Lys	Gly	
317						1035				1040			1045			
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320	Ile	His	Leu	Ile	Lys	His	Ala	Ile	Trp	Arg	Thr	Leu	Glu	Arg	Asn	

RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/539,723

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Input Set : N:\RJAVED\10539723.txt
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:48 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:28